AMENDMENTS TO THE SPECIFICATION

On page 1, immediately after the title, please insert the following paragraph:

This application is a divisional of U.S. Patent Application 09/533,798, filed March 24, 2000, which claims benefit of priority from U.S. Provisional Patent Applications 60/126,187, filed March 25, 1999, and 60/126,188, filed March 25, 1999, as well as PCT/GB99/03859, filed November 18, 1999 and designating the U.S.; all four applications are hereby incorporated by reference in their entireties as if fully set forth.

Please replace the paragraph and Tables 4 and 5 beginning at page 54, line 10 with the following new paragraph:

It is possible to modify human 5T4 to enhance its immunogenicity and thus induce more efficacious immunotherapy responses. ~~In order to~~ To do this, identification of HLA CTL epitopes and modification of such epitopes to improve binding to the HLA molecule, and [~~this~~] thus more efficient CTL induction, is performed using the programme "Peptide Binding Predictions" devised by K. Parker at the National ~~institutes of health http:www.bimas.dcrt.nih.gov/cgi binlmolbio/kenjarkercomboform (see Parker, K.C. *et al.* 1994. J. Immunol. 152:163)~~ Institutes of Health; <http:www.bimas.dcrt.nih.gov/cgi binlmolbio/kenjarkercomboform> (see Parker et al., *J. Immunol.*, 152:163 (1994)). The following results are obtained for human (Table 4) and murine (Table 5) 5T4 9mers:

Table 4: Human 5T4 9mers binding to HLA A 0201

Rank	Start	Sequence	Dissociation Time
1	97	FLTGNQLAV (SEQ ID NO:5)	319.939

2	364	ALIGAIFLL (SEQ ID NO:6)	284.974
3	351	SLQTSYVFL (SEQ ID NO:7)	176.240
4	368	AIFLLVLYL (SEQ ID NO:8)	137.482
5	283	GLPHIRVFL (SEQ ID NO:9)	117.493
6	358	FLGIVLALI (SEQ ID NO:10)	110.379
7	81	NLTEVPTDL (SEQ ID NO:11)	87.586
8	95	NLFLTGNQL (SEQ ID NO:12)	79.041
9	222	FLYLPRDVL (SEQ ID NO:13)	63.174
10	373	VLYLNRKGI (SEQ ID NO:14)	56.754
11	365	LIGAIFLLV (SEQ ID NO:15)	30.890
12	290	FLDNNPWVC (SEQ ID NO:16)	28.109
13	301	HMADMVTWL (SEQ ID NO:17)	27.207

Table 5: Murine 5T4 9mers binding to HLA A 0201

Rank	**Start**	**Sequence**	**Dissociation Time**
1	307	YMADMVAWL (SEQ ID NO:18)	3680.892
2	81	NLLEVPADL (SEQ ID NO:19)	324.068
3	97	FLTGNQMTV (SEQ ID NO:20)	319.939
4	370	ALIGAIFLL (SEQ ID NO:21)	284.974
5	228	FLFLPRDLL (SEQ ID NO:22)	178.158
6	357	SLQTSYVFL (SEQ ID NO:23)	176.240
7	374	AIFLLVLYL (SEQ ID NO:24)	137.482
8	289	GLAHVKVFL (SEQ ID NO:25)	117.493
9	364	FLGIVLALI (SEQ ID NO:26)	110.379
10	379	VLYLNRKG (SEQ ID NO:27)	56.754

Please replace the paragraph beginning at page 55, line 9 with the following new paragraph:

The above data derived from the Parker Peptide Binding Predictions Programme indicates that mutation of the human AA sequence starting at position 301 from **Y**MADMV**A**WL (SEQ ID NO: 18) when changed to **H**MADMV**T**WL (SEQ ID NO: 17) leads to a 10 fold increase in halftime of dissociation to HLA A0201. This increased binding affinity greatly improves the CTL induction properties of 5T4 polypeptides (see also Overwijk et al., 1998 J. Exp. Med. 188:277-86).